```
  1  GTGAAGGGAG CCGGGATCAG CCAGGGGCCA GCATGAGCCG GAGGGAGGGA AGTCTGGAAG ACCCCCAGAC TGATTCCTCA GTCTCACTTC TTCCCCACTT
     CACTTCCCTC GGCCCTAGTC GGTCCCCGGT CGTACTCCGC CTCCCTCCCT TCAGACCTTC TGGGGGTCTG ACTAAGGAGT CAGAGTGAAG AAGGGGTGAA
  1                                               M  S  R  R  E  G  G  S  L  E  D  P  Q  T  D  S  S  V  S  L  L  P  H  L
                                                  ^met

101  GGAGGCCAAG ATCCGTCAGA CACACAGCCT TGCGCACCTC CTCACCAAAT ACGCTGAGCA GCTGCTCCAG GAATATGTGC AGCTCCAGGG AGACCCCTTC
     CCTCCGGTTC TAGGCAGTCT GTGTGTCGGA ACGCGTGGAG GAGTGGTTTA TGCGACTCGT CGACGAGGTC CTTATACACG TCGAGGTCCC TCTGGGGAAG
 24   E  A  K  I  R  Q  T  H  S  L  A  H  L  L  T  K  Y  A  E  Q  L  L  Q  E  Y  V  Q  L  Q  G  D  P  F

201  GGGCTGCCCA GCTTCTCGCC GCCGCGGCTG CCGGTGGCCG GCCTGAGCGC CCCGGCTCCG AGCCACGCGG GGCTGCCAGT GCACGAGCCG CTGCGGCTGG
     CCCGACGGGT CGAAGAGCGG CGGCGCCGAC GGCCACCGGC CGGACTCGCG GGGCCGAGGC TCGGTGCGCC CCGACGGTCA CGTGCTCGGC GACGCCGACC
 57   G  L  P  S  F  S  P  P  R  L  P  V  A  G  L  S  A  P  A  P  S  H  A  G  L  P  V  H  E  R  L  R  L  D

301  ACGGCGGCGC GCTGGCCGCG CTGCCCCCGC TGCTGGACGC AGTGTGTCGC CGCCAGGCCG CGGCGCCGCC GCGCGCCCGC GCGGCGGACG CGGCGGACCT
     TGCCGCCGCG CGACCGGCGC GACGGGGGCG ACGACCTGCG TCACACAGCG GCGGTCCGGC GCCGCGGCGG CGCGCGGGCG CGCCGCCTGC GCCGCCTGGA
 91   A  A  A  L  A  A  L  P  P  L  D  A  V  C  R  R  Q  A  E  L  N  P  R  A  P  R  L  L  R  R  L  E

401  GGACGCGGCG CGCCAGGCCC GGGCCCCTGG GAGGCCTTGC CGCCGCCGTG AACCGCGGGC CCCGGGCCGA GCCCCCCGCC
     CCTGCGCCGC GCGGTCCGGG CCCGGGGACC CTCCGGAACG GCGGCGGCAC TTGGCGCCCG GGGCCCGGCT CGGGGGGCGG
124   D  A  A  R  Q  A  R  A  L  G  A  A  V  E  A  L  L  A  A  L  G  A  A  N  R  G  P  R  A  E  P  P  A

501  GCCACCGCCT CAGCCCGCTC CGCCACCGGG GTCTTCCCCG CCAAGGTGCT GGGGCTCCGC GTTTGCGGCC TCTACCGCGA GTGGCTGAGC CGCACCGAGG
     CGGTGGCGGA GTCGGGCGAG GCGGTGGCCC CAGAAGGGGC GGTTCCACGA CCCCGAGGCG CAAACGCCGG AGATGGCGCT CACCGACTCG GCGTGGCTCC
157   A  T  A  S  A  A  S  A  T  G  V  F  P  A  K  V  L  G  L  R  V  C  G  L  Y  R  E  W  L  S  R  T  E  G

601  GCGACCTGGG CCAGCTGCTG CCCGGGGGCT CGGCCTGAGC GCCGCGGGGC GCCGCGCCCC AGCTCGCCCC GCCTCCTCCC GTCTCTCCTT CCGCTTCTTT
     CGCTGGACCC GGTCGACGAC GGGCCCCCGA GCCGGACTCG CGGCGCCCCG CGGCGCGGGG TCGAGCGGGG CGGAGGAGGG CAGAGAGGAA GGCGAAGAAA
191   D  L  G  Q  L  L  P  G  G  S  A  O  (SEQ ID NO:3)

701  GTCTTTCTCT GCCGCTGTCG GTGTCTGTCT AGCTGTCTCT ATTGCCTCGG CCTTCTTTGC TTTTTGTGGG GGAGAGGGGA GGGGACGGGC
     CAGAAAGAGA CGGCGACAGC CACAGACAGA TCGACAGAGA TAACGGAGCC GGAAGAAACG AAAAACACCC CCTCTCCCCT CCCCTGCCCG

801  AGGGTCTCTG TCGCCCAGGC TGGGGTGCAG TGGCGCGATC CCAGCACTGC AGCCTCAACC TCCTGGGCTC AGCCTCCCAG CTTCCCCAGC
     TCCCAGAGAC AGCGGGTCCG ACCCCCACGTC ACCGGCGCTAG GGTCGTGACG TCGGAGTTGG AGGACCCGAG TCGGAGGGTCG
```

FIG. 1A

13

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901  AGCTGGGACT ACAGGCACGC GCCACCACAG CCGGCTAATT TTTTATTTAA TTTTTTGTAG AGACGAGGTT TCGCCATGTT GCCCAGGCTG GTCTTGAACT
     TCGACCCTGA TGTCCGTGCG CGGTGGTGTC GGCCGATTAA AAAAAACATC TCTGCTCCAA AGCGGTACAA CGGGTCCGAC CAGAACTTGA

1001 CCGGGGCTCA AGCGATCCTC CCGCTTCAGC CTCCCTAAGT GCTGGGATTG CAGGCGTGAG CCACTTTCCC AGCCTCTCTT TGCTTTGCCT GCCCCGTTCT
     GGCCCCGAGT TCGCTAGGAG GGCGAAGTCG GAGGGATTCA CGACCCTAAC GTCCGCACTC GGTGAAAGGG TCGGAGAGAA ACGAAACGGA CGGGGCAAGA
         ^58125.tm.f1                                                                                 ^58125.tm.p1

1101 CTTAACTCTT GGACCCTCCT CGTCTGCATG GTAACTCCGT CTGAGTCTAC CATTTTCTTG CTCTCCCTCC TTCCTTGGGC CTGCCTCAGT TCCCTTTGGC
     GAATTGAGAA CCTGGGAGGA GCAGACGTAC CATTGAGGCA GACTCAGATG GTAAAAGAAC GAGAGGGAGG AAGGAACCCG GACGGAGTCA AGGGAAACCG
         ^58125.tm.r1

1201 CTCCCCCTTT ACCCAGCTCT TGGGGTGTCT CTGTTTTTTC CATCCCCACT TCCTGCCTTC TCGTGGCCCT GTGTGAGCAC ATGTGTACAT CTCAGCCTTA
     GAGGGGGAAA TGGGTCGAGA ACCCCACAGA GACAAAAAAG GTAGGGGTGA AGGACGGAAG AGCACCGGGA CACACTCGTG TACACATGTA GAGTCGGAAT

1301 TCTCAAGGAG GTGACACCTT CTCTCCTTGT CCCCATCTGG CCGTCTCTCT GTGCTTCCCT GGCCAGGGGC GTGCCTGCTG GGGAAGGCTA
     AGAGTTCCTC CACTGTGGAA GAGAGGAACA GGGGTAGACC GGCAGAGAGA CACGAAGGGA CCGGTCCCCG CACGGACGAC CCCTTCCGAT

1401 CTCCGCATCT CAGCCACTTT CCTCAGGCTC ACTCCACCTA CATCCCCAGT CTGCCACACC CCATCCCTTT GGGCCTCAGC CCTGTCCCTT TGATGTCCTC
     GAGGCGTAGA GTCGGTGGAA GGAGTCCGAG TGAGGTGGAT GTAGGGGTCA GACGGTGTGG GGTAGGGAAA CCCGGAGTCG GGACAGGGAA ACTACAGGAG

1501 CTTTCCTTCA GCCCCTCTGC CCTGTCCCTG CACACCTCC   (SEQ ID NO:1)
     GAAAGGAAGT CGGGGAGACG GGACAGGGAC GTGTGGAGG   (SEQ ID NO:2)
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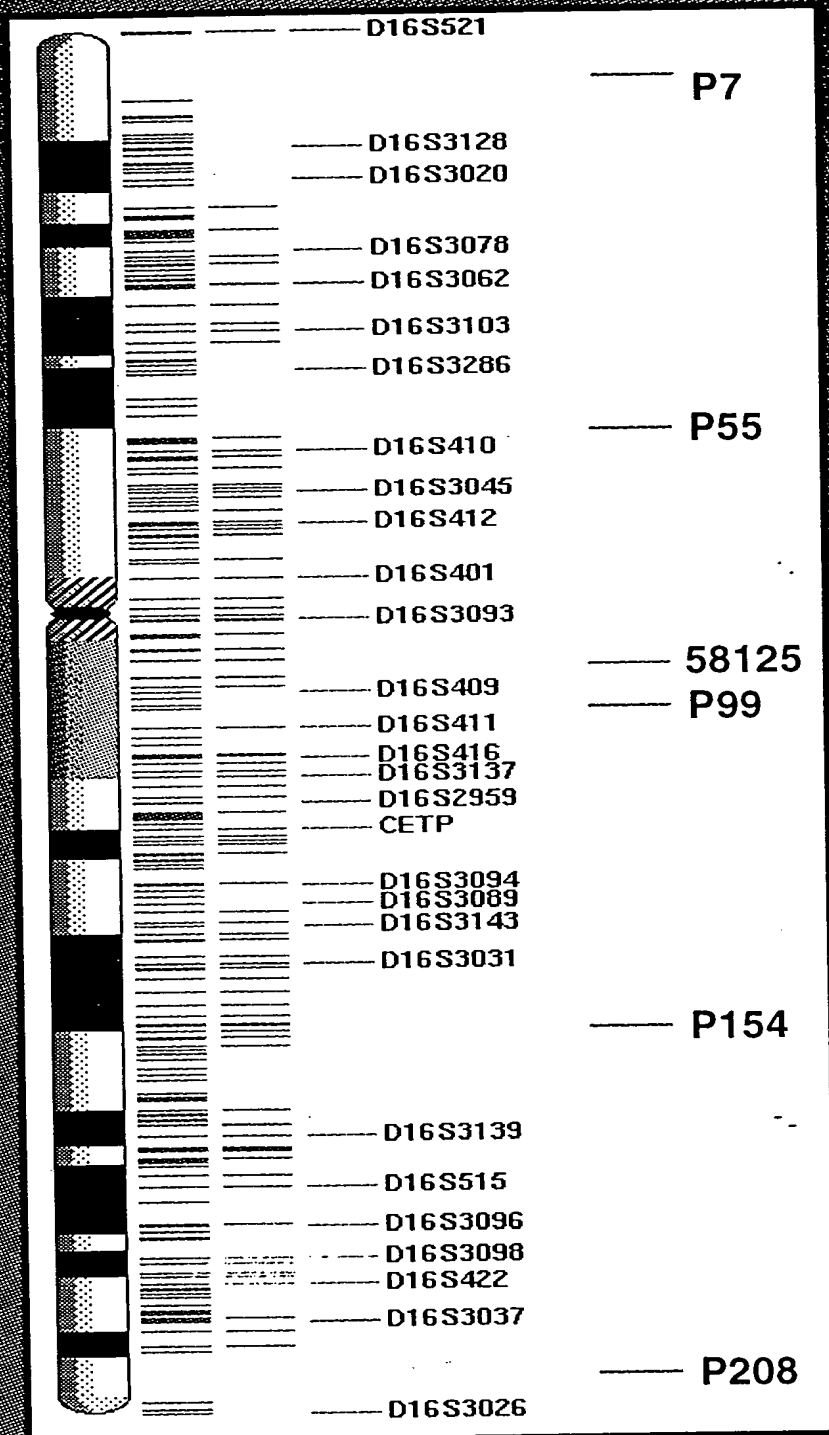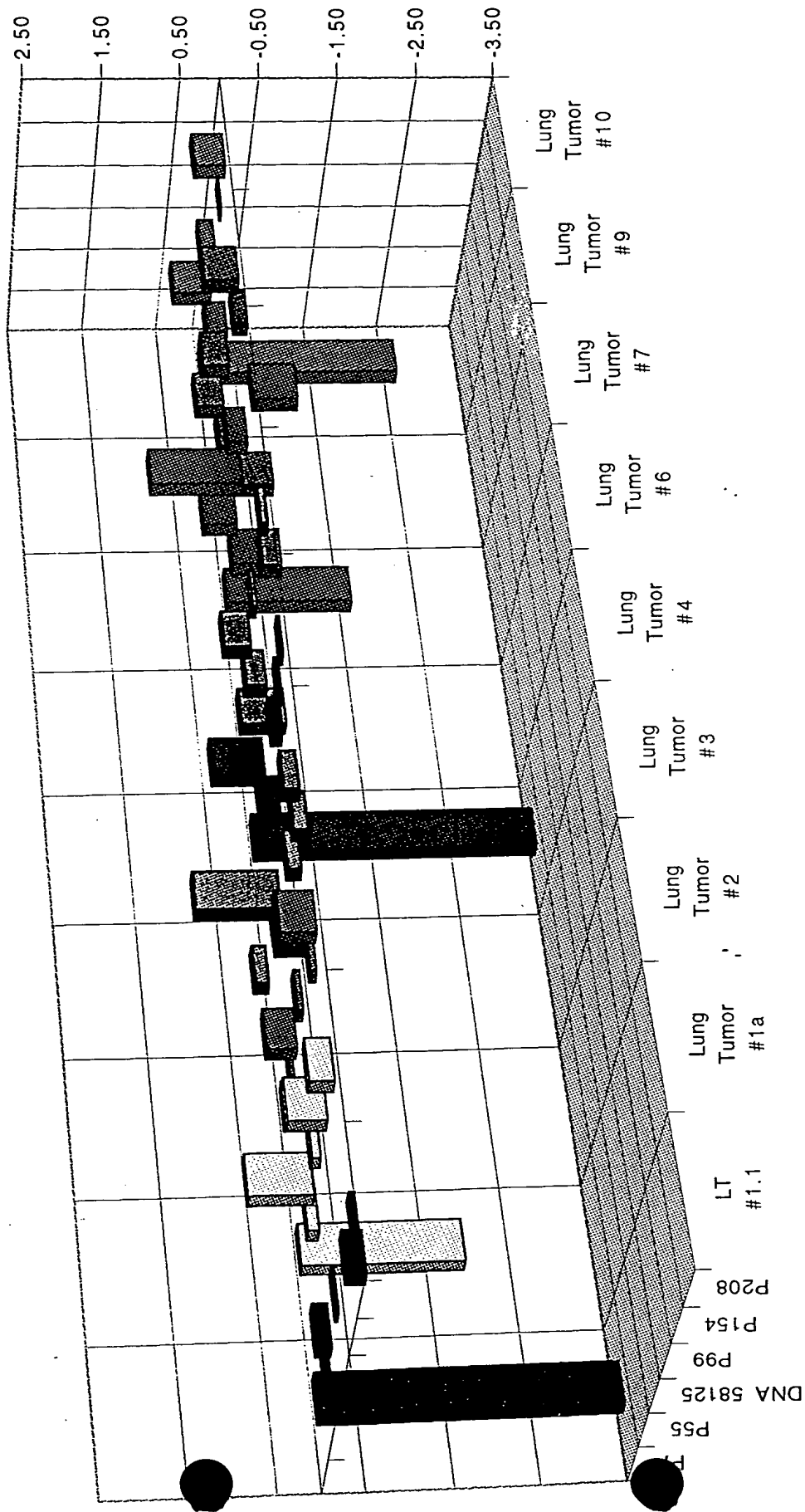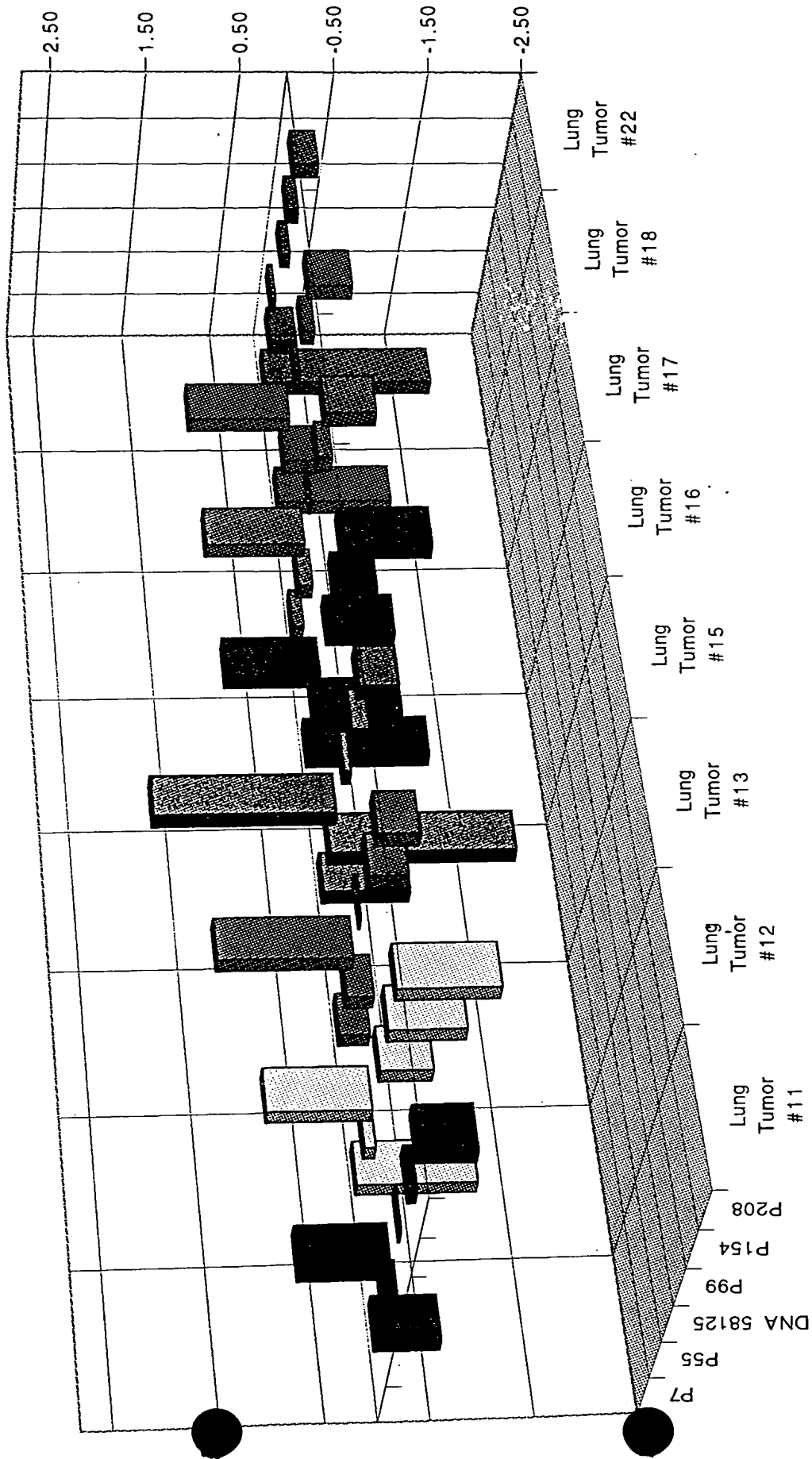
FIG. 1B

FIG. 2

Framework Analysis of DNA58125 Cardiotrophin-1
on Lung Tumor Panel 1

FIG. 3

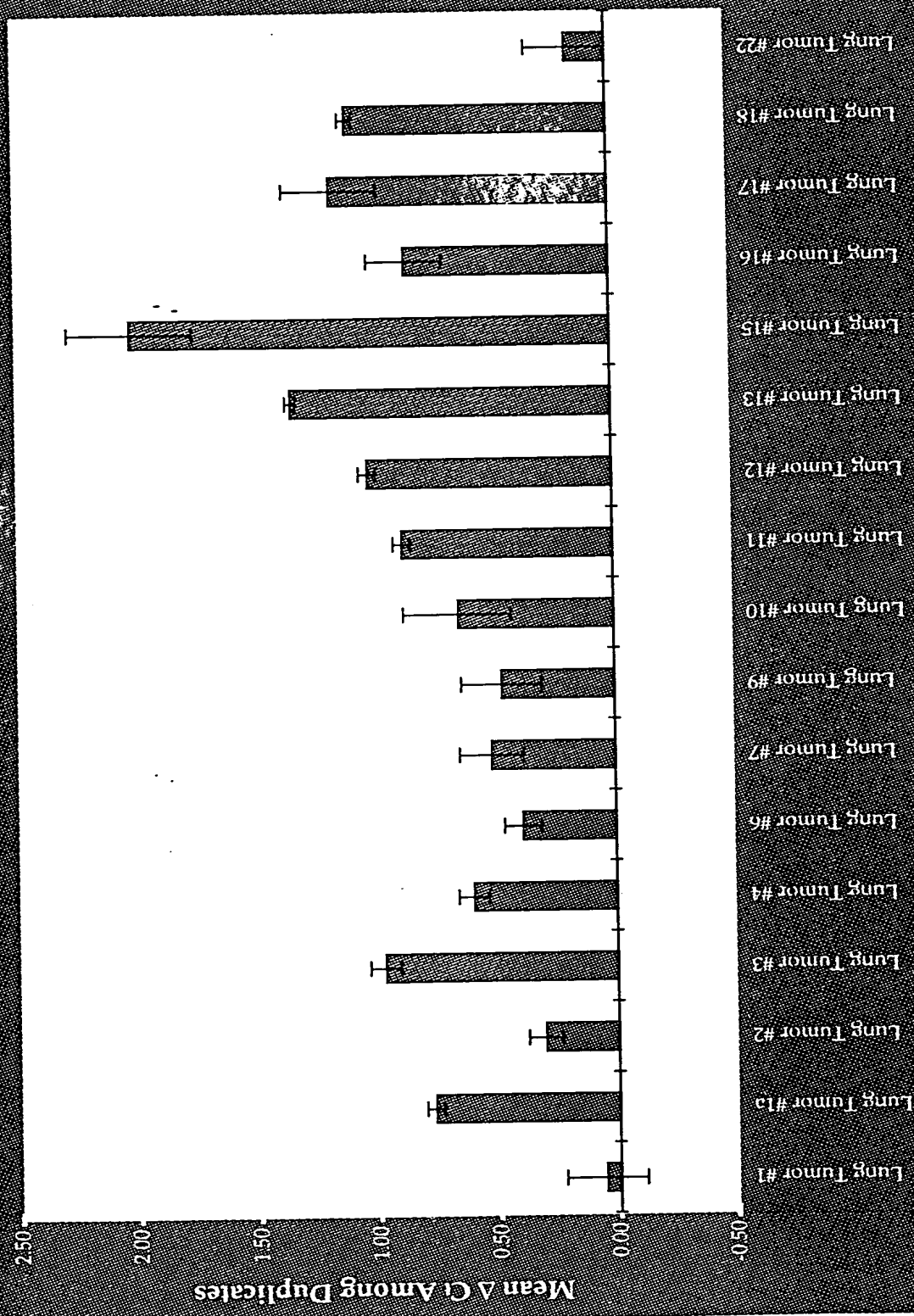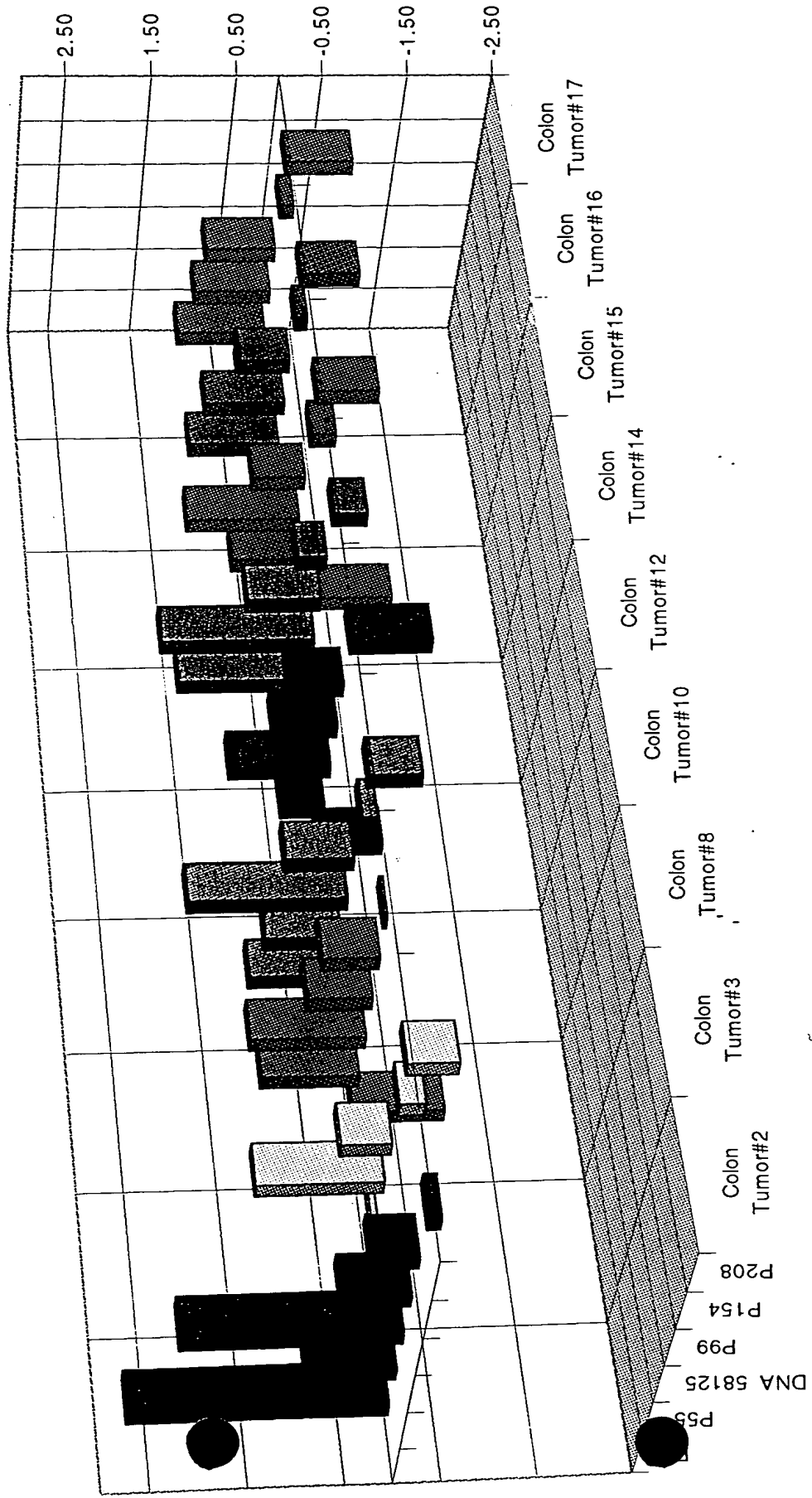**Framework Analysis of DNA58125 Cardiotrophin-1 on Lung Tumor Panel 2**

F/G. 4

FIG. 5

DNA 58125 (CK1)
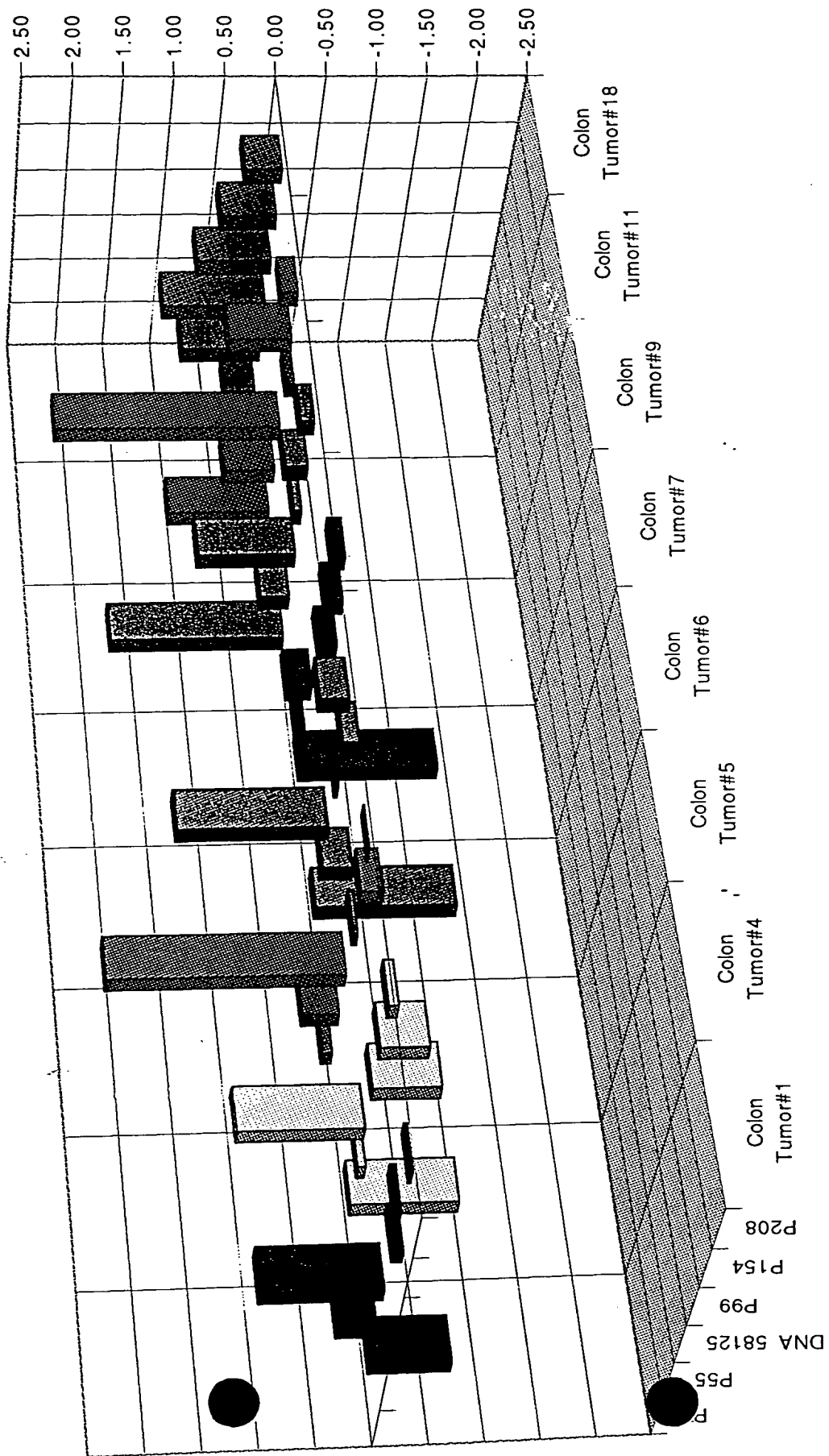on Lung Tumor Panels 1&2

Lung Tumor Panels 1&2

Mean Δ Ct Among Duplicates

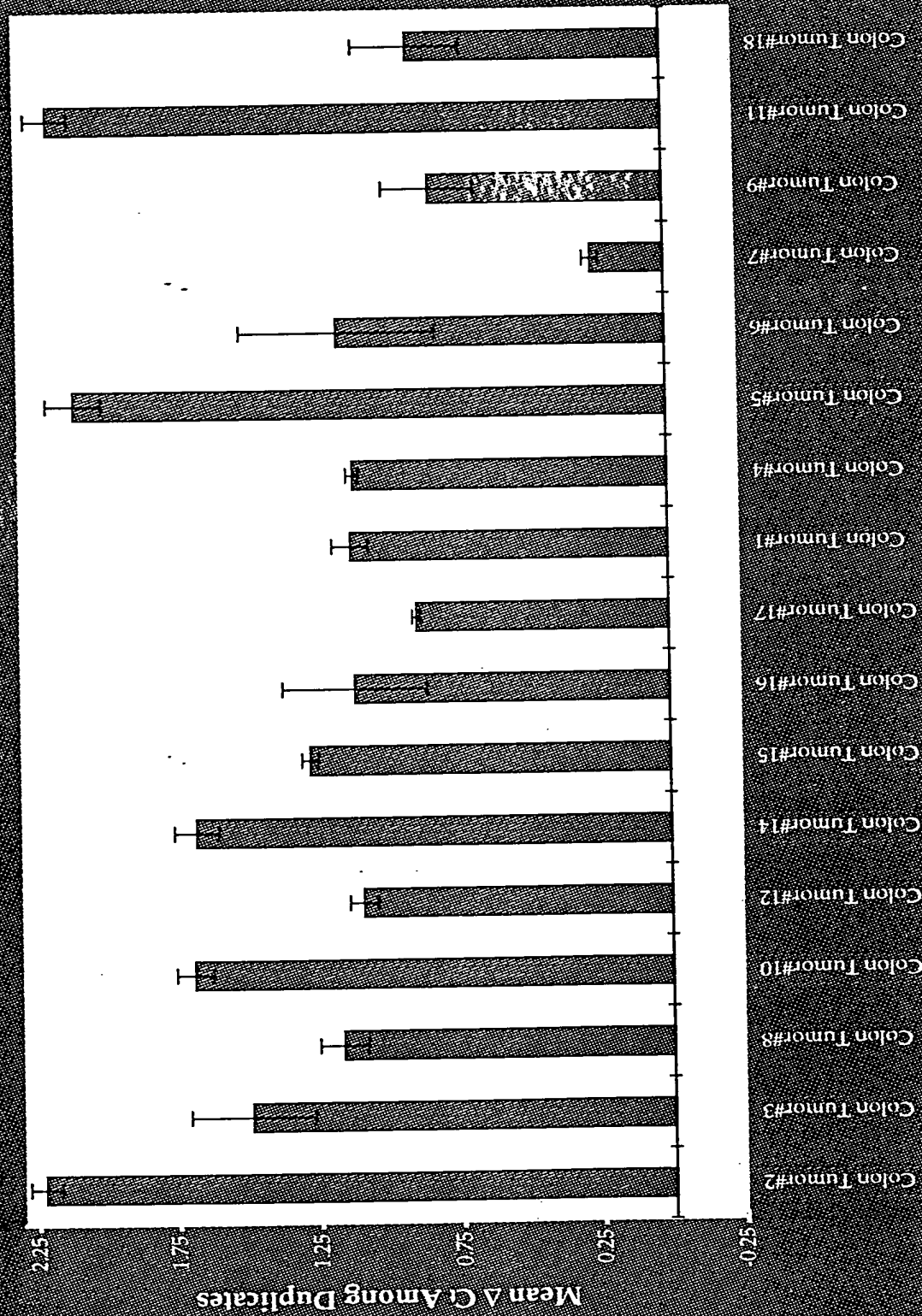Framework Analysis of DNA58125 Cardiotrophin-1
on Colon Tumor Panel #1

FIG. 6

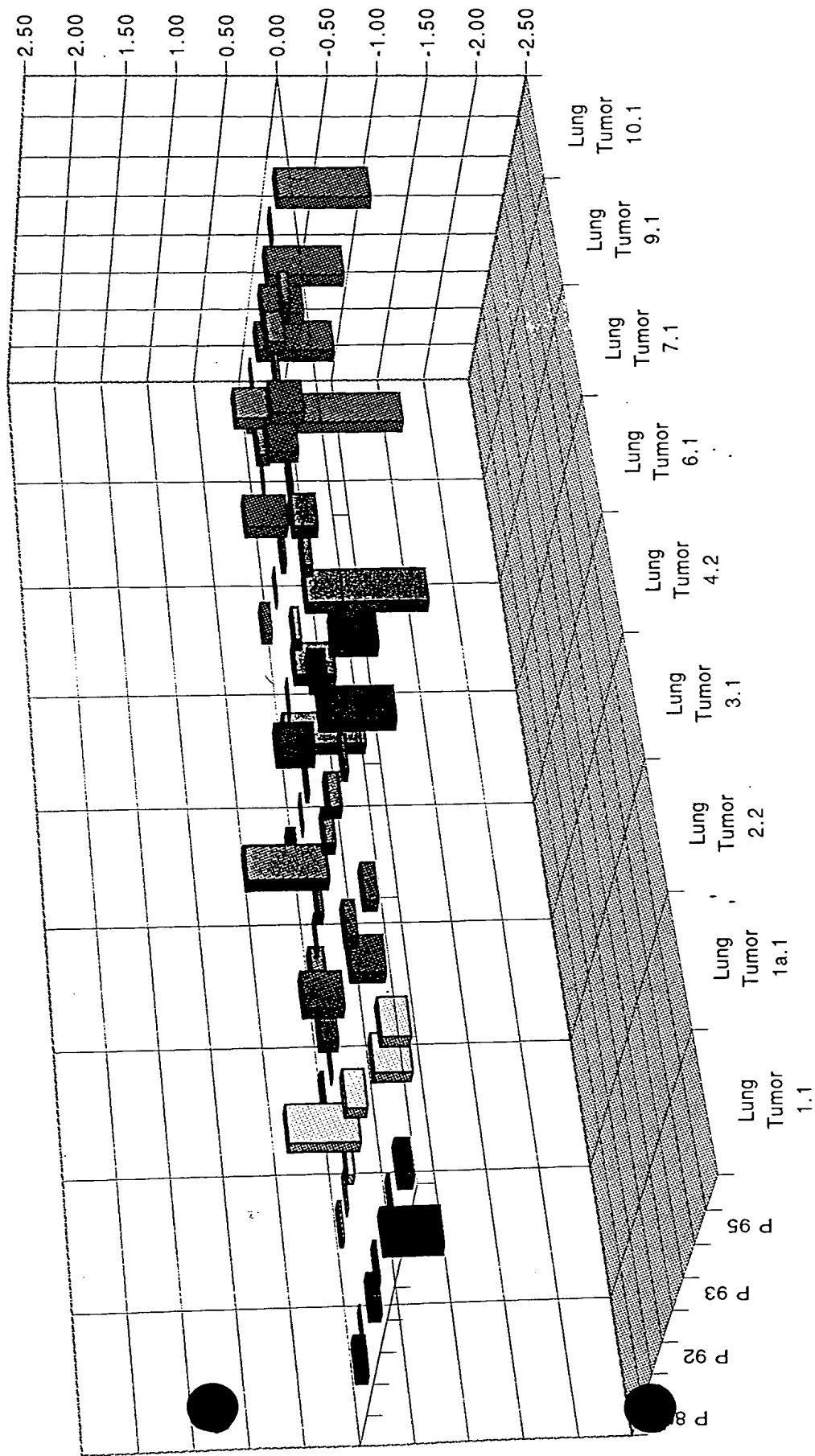Framework Analysis of DNA58125 Cardiotrophin-1
on Colon Tumor Panel 2
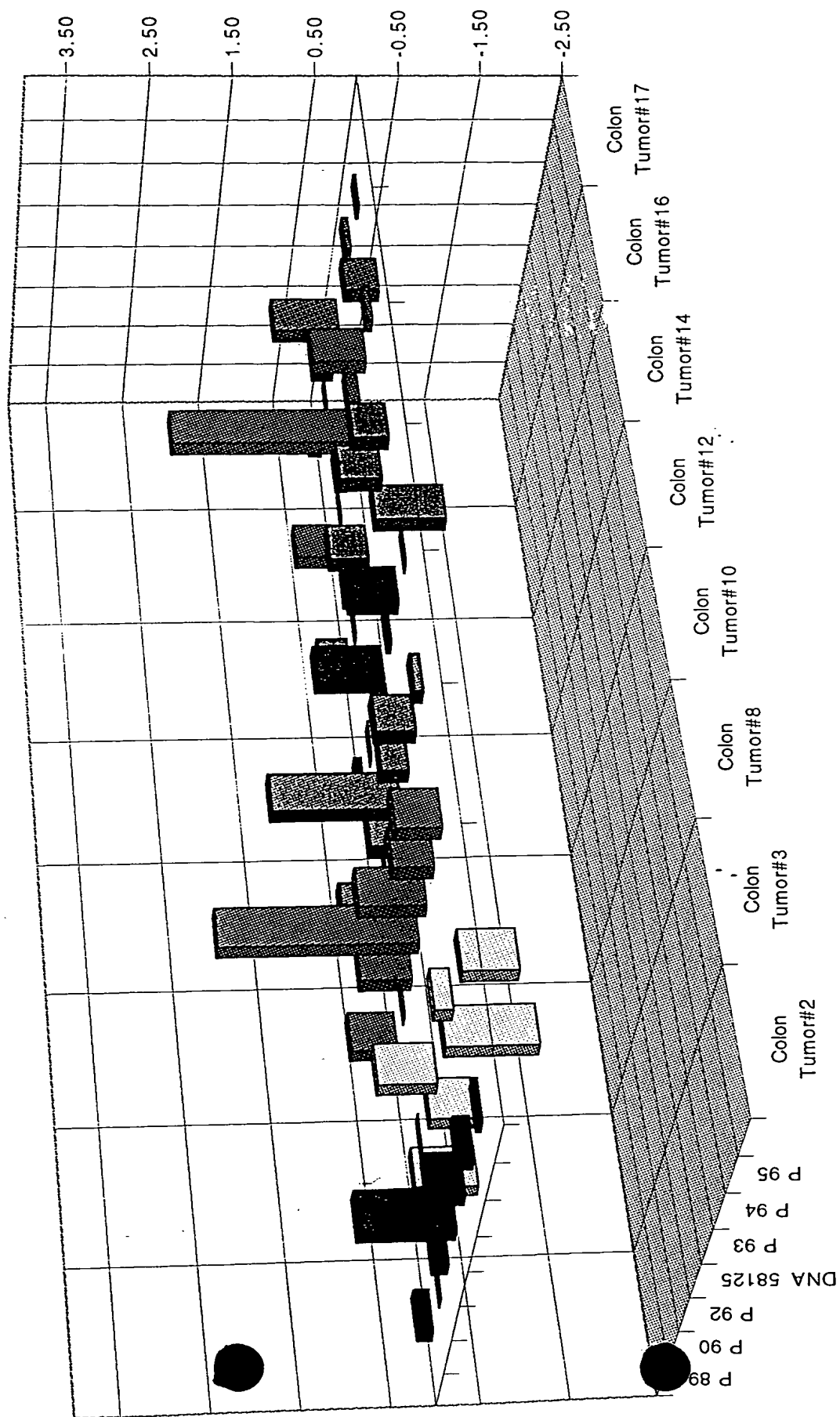
FIG. 7

FIG. 8

DNA 58125 (CT-1)
on Colon Tumor Panels 1&2

Mean Δ Ct Among Duplicates

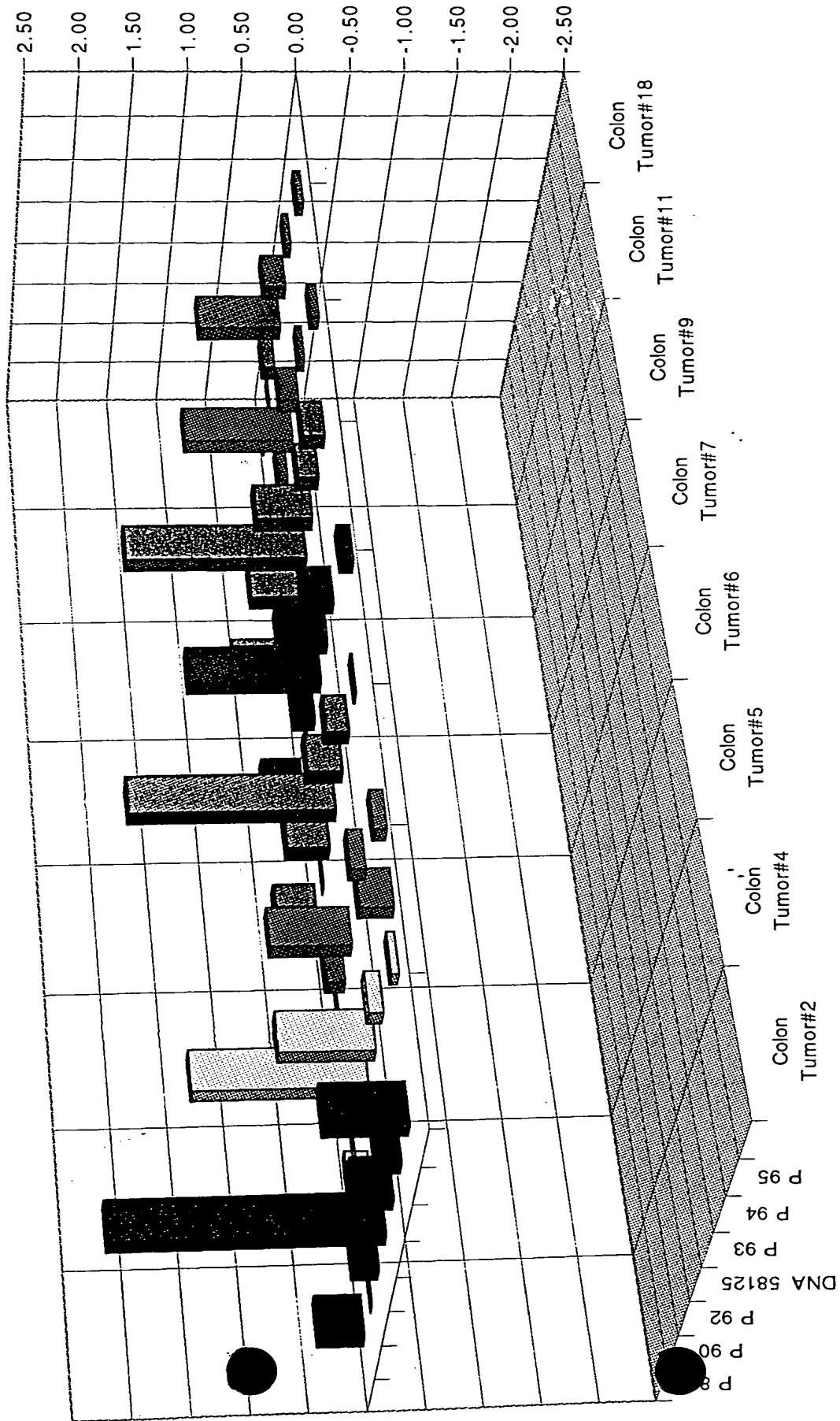Colon Tumor Panels 1&2

Colon Tumor#2
Colon Tumor#3
Colon Tumor#8
Colon Tumor#10
Colon Tumor#12
Colon Tumor#14
Colon Tumor#15
Colon Tumor#16
Colon Tumor#17
Colon Tumor#1
Colon Tumor#4
Colon Tumor#5
Colon Tumor#6
Colon Tumor#7
Colon Tumor#9
Colon Tumor#11
Colon Tumor#18

Lung Tumor Panel #1
Epicenter for Chromosome # 16

FIG. 9

US 2003/0082565 A1

Lung Tumor Panel #2
Epicenter for Chromosome # 16

FIG. 1D

0.5/6/3 . 032000

Colon Tumor Panel #1
Epicenter for Chromosome # 16

FIG. 17

FIG.17 082500

Colon Tumor Panel #2
Epicenter for Chromosome # 16

FIG. 13